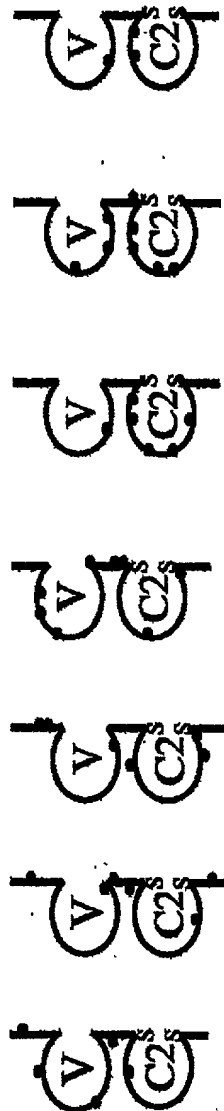


CD2 CD58 CD48 SLAM APEX-1 APEX-2 APEX-3



• = potential N-linked glycosylation sites

FIGURE 1

GGAAGTGGCTTCATTTAGTGGCTGACTTCCAGAGAGCAAT 41
 ATGGCTGGTTCCCCAACATGCCTCACCTCATCTATATCCTTTGGCAGCTCACAGGGTCA 101
M A G S P T C L T L I Y I L W Q L T G S 20
 GCAGCCTCTGGACCCGTGAAAGAGCTGGTCGGTTCCGTTGGTGGGGCCGTGACTTTCCCC 161
A A S G P V K E L V G S V G G A V T F P 40
 CTGAAGTCCAAAGTAAAGCAAGTTGACTCTATTGTCTGGACCTTCAACACAACCCCTCTT 221
 L K S K V K Q V D S I V W T F N T T P L 60
 GTCACCATACAGCCAGAAGGGGGCACTATCATAGTGACCCAAATCGTAATAGGGAGAGA 281
 V T I Q P E G G T I I V T Q N R N R E R 80
 GTAGACTTCCAGATGGAGGCTACTCCCTGAAGCTCAGCAAAGTGAAGAAGTACTCA 341
 V D F P D G G Y S L K L S K L K K N D S 100
 GGGATCTACTATGTGGGGATATACAGCTCATCACTCCAGCAGCCCTCCACCCAGGAGTAC 401
 G I Y Y V G I Y S S L Q Q P S T Q E Y 120
 GTGTGCATGTCTACGAGCACCTGTCAAAGCCTAAAGTCACCATGGGTCTGCAGAGCAAT 461
 V L H V Y E H L S K P K V T M G L Q S N 140
 AAGAATGGCACCTGTGTGACCAATCTGACATGCTGCATGGAACATGGGAAGAGGATGTG 521
 K N G T C V T N L T C C M E H G E E D V 160
 ATTTATACCTGGAAGGCCCTGGGGCAAGCAGCCAATGAGTCCCATATGGGTCCATCCTC 581
 I Y T W K A L G Q A A N E S H N G S I L 180
 CCCATCTCCTGGAGATGGGGAGAAAGTGATATGACCTTCATCTGCGTTGCCAGGAACCT 641
 P I S W R W G E S D M T F I C V A R N P 200
 GTCAGCAGAACTTCTCAAGCCCCATCCTTGCCAGGAAGCTCTGTGAAGGTGCTGTGTAT 701
 V S R N E S S P I L A R K L C E G A A D 220
 GACCCAGATTCCTCCATGGTCTCTCTGTCTCTCTGTGGTGGCCCTCTGCTCAGTCTC 761
 D P D S S M V L L L C L L L V P L L L S L 240
 TTTGTACTGGGGCTATTTCTTTGGTTTCTGAAGAGAGAGAGACAAGAAGGTACATTGAA 821
F V L G L F L W F L K R E R Q E E Y I E 260
 GAGAAGAAGAGAGTGGACATTTGTGCGGAAACTCCTAACATATGCCCCATTCTGGAGAG 881
 E K K R V D I C R E T P N I C P H S G E 280
 AACACAGAGTACGACACAATCCCTCACACTAATAGAACAATCCTAAAGGAAGATCCAGCA 941
 N T E Y D T I P H T N R T I L K E D P A 300
 AATACGGTTTACTCCACTGTGGAATACCGAAAAAGATGAAAAATCCCCACTCACTGCTC 1001
 N T V Y S T V E I P K K M E N P H S L L 320
 ACGATGCCAGACACACCAAGGCTATTTGCCTATGAGAATGTTATCTAGACAGCAGTGCAC 1061
 T M P D T P R L F A Y E N V I * 335
 TCCCTAAGTCTCTGCTCAAAAAAACAATTTCTCGGCCCAAGAAAAACAATCAGAAGA 1121
 ATTCATGATTGACTAGAAACATCAAGGAAGATGAAGAACGTTGACTTTTTTCCAGGA 1181
 TAAATTATCTCTGATGCTTCTTTAGATTTAAGAGTTCGTAATTCATCCACTGCTGAGAA 1241
 ATCTCCTCAAACCCAGAAGGTTAATCACTTCATCCCAAAATGGGATTGTGAATGTCAG 1301
 CAAACCATAAAAAAAGTGCTTAGAAGTATTCCTATAGAATGTAAATGCAAGGTCACACA 1361
 TATTAATGACAGCCTGTTGTATTAATGATGGCTCCAGGTCAGTCTGGAGTTTCATTCC 1421
 ATCCCAGGGCTTGGATGTGAGGATATACCAAGAGTCTTGCTACCAGGAGGGCAAGAAGA 1481
 CCAAAACAGACAGACAAGTCCAGCAGAAGCAGATGCACCTGACAAAAATGGATGTATTAA 1541
 TTGGCTCTATAAACTATGTGCCAGCACTATGCTGAGCTTACCTAATTTGGTCAGACGTG 1601
 CTGTCTGCCCTCATGAATTTGGCTCCAAATGAATGAACACTTTTCATGAGCAGTTGTAGC 1661
 AGGCCTGACCACAGATTCCCAGAGGGCCAGGTGTGGATCCACAGGACTTGAAGTCAAAG 1721
 TTCACAAAGATGAAGAATCAGGGGTAGCTGACCATGTTTGGCAGATACTATAATGGAGACA 1781
 CAGAAGTGTGCATGGCCCAAGGACAAGGACCTCCAGCCAGGCTTCATTTATGCATTGTG 1841
 CTGCAAAAGAAAAGTCTAGGTTTTAAGGCTGTGCCAGAACCATCCCAATAAGAGACCG 1901
 AGTCTGAAGTCACATTGTAATCTAGTGTAGGAGACTTGGAGTCAGGCAGTGAGACTGGT 1961
 GGGGCACGGGGGGCAGTGGGTACTTGTAACCTTTAAAGATGGTTAATTCATTCAATAGA 2021
 TATTTATTAAGAACCTACTATGCGGGCCGGCATGGTGGCTCACACCTGTAATCCAGCAC 2081
 TTTGGGAGGCCAAGGTGGGTGGGTCTGAGGTGAGGTTCAAGACCAGCCTGGCCAA 2141
 CATGGTGAAACCCATCTCTACTAAAGATCAAAATTTGCTGAGCGTGGTGGTGTGCACCT 2201

FIGURE 2

1990 1991 1992 1993 1994 1995 1996 1997 1998 1999 2000 2001 2002 2003 2004 2005 2006 2007 2008 2009 2010 2011 2012 2013 2014 2015 2016 2017 2018 2019 2020 2021 2022 2023 2024 2025 2026 2027 2028 2029 2030 2031 2032 2033 2034 2035 2036 2037 2038 2039 2040 2041 2042 2043 2044 2045 2046 2047 2048 2049 2050 2051 2052 2053 2054 2055 2056 2057 2058 2059 2060 2061 2062 2063 2064 2065 2066 2067 2068 2069 2070 2071 2072 2073 2074 2075 2076 2077 2078 2079 2080 2081 2082 2083 2084 2085 2086 2087 2088 2089 2090 2091 2092 2093 2094 2095 2096 2097 2098 2099 2100 2101 2102 2103 2104 2105 2106 2107 2108 2109 2110 2111 2112 2113 2114 2115 2116 2117 2118 2119 2120 2121 2122 2123 2124 2125 2126 2127 2128 2129 2130 2131 2132 2133 2134 2135 2136 2137 2138 2139 2140 2141 2142 2143 2144 2145 2146 2147 2148 2149 2150 2151 2152 2153 2154 2155 2156 2157 2158 2159 2160 2161 2162 2163 2164 2165 2166 2167 2168 2169 2170 2171 2172 2173 2174 2175 2176 2177 2178 2179 2180 2181 2182 2183 2184 2185 2186 2187 2188 2189 2190 2191 2192 2193 2194 2195 2196 2197 2198 2199 2200 2201 2202 2203 2204 2205 2206 2207 2208 2209 2210 2211 2212 2213 2214 2215 2216 2217 2218 2219 2220 2221 2222 2223 2224 2225 2226 2227 2228 2229 2230 2231 2232 2233 2234 2235 2236 2237 2238 2239 2240 2241 2242 2243 2244 2245 2246 2247 2248 2249 2250 2251 2252 2253 2254 2255 2256 2257 2258 2259 2260 2261 2262 2263 2264 2265 2266 2267 2268 2269 2270 2271 2272 2273 2274 2275 2276 2277 2278 2279 2280 2281 2282 2283 2284 2285 2286 2287 2288 2289 2290 2291 2292 2293 2294 2295 2296 2297 2298 2299 2300 2301 2302 2303 2304 2305 2306 2307 2308 2309 2310 2311 2312 2313 2314 2315 2316 2317 2318 2319 2320 2321 2322 2323 2324 2325 2326 2327 2328 2329 2330 2331 2332 2333 2334 2335 2336 2337 2338 2339 2340 2341 2342 2343 2344 2345 2346 2347 2348 2349 2350 2351 2352 2353 2354 2355 2356 2357 2358 2359 2360 2361 2362 2363 2364 2365 2366 2367 2368 2369 2370 2371 2372 2373 2374 2375 2376 2377 2378 2379 2380 2381 2382 2383 2384 2385 2386 2387 2388 2389 2390 2391 2392 2393 2394 2395 2396 2397 2398 2399 2400 2401 2402 2403 2404 2405 2406 2407 2408 2409 2410 2411 2412 2413 2414 2415 2416 2417 2418 2419 2420 2421 2422 2423 2424 2425 2426 2427 2428 2429 2430 2431 2432 2433 2434 2435 2436 2437 2438 2439 2440 2441 2442 	
--	--

FIGURE 2 (continued)

1 CCATCCTAATACGACTCACTATAGGGCTCGAGCGGCCGCCCGGGCAGGTTTCAAGTTCCA
 -----+-----+-----+-----+-----+-----+-----+
 61 CGTTCCCTACTGCTAAGAGTCTTAGCTTACAAAAGATATTCTTGTAAGCCAAGTGTGAAG
 -----+-----+-----+-----+-----+-----+-----+
 121 TTAATCACGACAACCAAAGGTTTGCTAACATAGAGGAAGAGCTCTCATCAATAGGGGAAC
 -----+-----+-----+-----+-----+-----+-----+
 181 AGAAAGTCTCAGCGACAAGCTTATGAAAGAATGGCTGTCTCAAGGGCTCCAACACCCGAC
 -----+-----+-----+-----+-----+-----+-----+
 M A V S R A P T P D
 241 TCCGCCTGTCAGAGGATGGTCTGGCTCTTTCCACTTGTCTTCTGCCTCGGCTCAGGGAGT
 -----+-----+-----+-----+-----+-----+-----+
 S A C Q R M V W L F P L V F C L G S G S
 301 GAAGTTTCACAGAGCAGCTCAGACCCCCAGCTAATGAATGGCGTTCTAGGAGAGTCTGCA
 -----+-----+-----+-----+-----+-----+-----+
 E V S Q S S S D P Q L M N G V L G E S A
 361 GTTCTTCCTCTAAAGCTTCCTGCAGGGAAGATAGCCAATATCATCATCTGGAATTATGAA
 -----+-----+-----+-----+-----+-----+-----+
 V L P L K L P A G K I A N I I I W N Y E
 421 TGGGAAGCGTCACAAGTCACTGCCCTCGTTATCAACCTAAGTAATCCTGAAAGTCCACAA
 -----+-----+-----+-----+-----+-----+-----+
 W E A S Q V T A L V I N L S N P E S P Q
 481 ATCATGAACACTGATGTAAAGAAGAGACTGAACATCACCCAGTCCTACTCCCTGCAAATC
 -----+-----+-----+-----+-----+-----+-----+
 I M N T D V K K R L N I T Q S Y S L Q I
 541 AGCAACCTTACCATGGCAGACACAGGATCATACACTGCGCAGATAACCACAAAGGACTCT
 -----+-----+-----+-----+-----+-----+-----+
 S N L T M A D T G S Y T A Q I T T K D S
 601 GAAGTGATCACCTTCAAATATATTCTGAGGGTCTTTGAACGATTGGGTAACTTAGAAACT
 -----+-----+-----+-----+-----+-----+-----+
 E V I T F K Y I L R V F E R L G N L E T

FIGURE 3

661 ACCAACTATACTCTCCTGCTAGAGAATGGGACCTGCCAGATACACCTGGCCTGTGTTTTG
 -----+-----+-----+-----+-----+
 T N Y T L L L E N G T C Q I H L A C V L

721 AAGAATCAAAGTCAAACGTCTCAGTTGAGTGGCAAGCCACAGGAAACATCTCTTTAGGA
 -----+-----+-----+-----+-----+
 K N Q S Q T V S V E W Q A T G N I S L G

781 GGACCAAATGTCACTATCTTTTGGGACCCGAGGAATTCTGGTGACCAGACTTACGTCTGC
 -----+-----+-----+-----+-----+
 G P N V T I F W D P R N S G D Q T Y V C

841 AGAGCCAAGAATGCTGTCAGCAATTTGTCAGTCTCTGTTTCGACCCAGAGTCTCTGCAAA
 -----+-----+-----+-----+-----+
 R A K N A V S N L S V S V S T Q S L C K

901 GGGGTTCTAACTAATCCACCCTGGAATGCAGTATGGTTTATGACTACAATTTCAATAATC
 -----+-----+-----+-----+-----+
 G V L T N P P W N A V W F M T T I S I I

961 AGTGCAGTCATACTCATCTTTGTGTGCTGGAGCATA CATGTTTGAAGAGAAGAGGTCT
 -----+-----+-----+-----+-----+
 S A V I L I F V C W S I H V W K R R G S

1021 CTCCTTTGACTAGCCAACATCCAGAGTCTCCCAGAGCACAGATGGCCCAGGCTCTCCA
 -----+-----+-----+-----+-----+
 L P L T S Q H P E S S Q S T D G P G S P

1081 GGGAACACTGTGTATGCACAAGTCACTCGTCCAATGCAGGAAATGAAAATCCCCAAAACCT
 -----+-----+-----+-----+-----+
 G N T V Y A Q V T R P M Q E M K I P K P

1141 ATCAAAAATGACTCCATGACAATTTACTCCATAGTTAATCATTCCAGAGAGGAAACAGTG
 -----+-----+-----+-----+-----+
 I K N D S M T I Y S I V N H S R E E T V

1201 GCTTTAACCGGCTATAACCAACCCATTACCCTGAAGGTTAACACTTTAATCAACTATAAC
 -----+-----+-----+-----+-----+
 A L T G Y N Q P I T L K V N T L I N Y N

1261 TCCTGAAGGAAGAGCACTGCAGTGACTTGAGGAAATTAAACAATGCTGTCACCACAGCTC
 -----+-----+-----+-----+-----+
 S *

FIGURE 3 (continued)

1997 1998 1999 2000 2001 2002 2003 2004 2005 2006 2007 2008 2009 2010 2011 2012 2013 2014 2015 2016 2017 2018 2019 2020 2021 2022 2023 2024 2025 2026 2027 2028 2029 2030 2031 2032 2033 2034 2035 2036 2037 2038 2039 2040 2041 2042 2043 2044 2045 2046 2047 2048 2049 2050 2051 2052 2053 2054 2055 2056 2057 2058 2059 2060 2061 2062 2063 2064 2065 2066 2067 2068 2069 2070 2071 2072 2073 2074 2075 2076 2077 2078 2079 2080 2081 2082 2083 2084 2085 2086 2087 2088 2089 2090 2091 2092 2093 2094 2095 2096 2097 2098 2099 2100 2101 2102 2103 2104 2105 2106 2107 2108 2109 2110 2111 2112 2113 2114 2115 2116 2117 2118 2119 2120 2121 2122 2123 2124 2125 2126 2127 2128 2129 2130 2131 2132 2133 2134 2135 2136 2137 2138 2139 2140 2141 2142 2143 2144 2145 2146 2147 2148 2149 2150 2151 2152 2153 2154 2155 2156 2157 2158 2159 2160 2161 2162 2163 2164 2165 2166 2167 2168 2169 2170 2171 2172 2173 2174 2175 2176 2177 2178 2179 2180 2181 2182 2183 2184 2185 2186 2187 2188 2189 2190 2191 2192 2193 2194 2195 2196 2197 2198 2199 2200 2201 2202 2203 2204 2205 2206 2207 2208 2209 2210 2211 2212 2213 2214 2215 2216 2217 2218 2219 2220 2221 2222 2223 2224 2225 2226 2227 2228 2229 2230 2231 2232 2233 2234 2235 2236 2237 2238 2239 2240 2241 2242 2243 2244 2245 2246 2247 2248 2249 2250 2251 2252 2253 2254 2255 2256 2257 2258 2259 2260 2261 2262 2263 2264 2265 2266 2267 2268 2269 2270 2271 2272 2273 2274 2275 2276 2277 2278 2279 2280 2281 2282 2283 2284 2285 2286 2287 2288 2289 2290 2291 2292 2293 2294 2295 2296 2297 2298 2299 2300 2301 2302 2303 2304 2305 2306 2307 2308 2309 2310 2311 2312 2313 2314 2315 2316 2317 2318 2319 2320 2321 2322 2323 2324 2325 2326 2327 2328 2329 2330 2331 2332 2333 2334 2335 2336 2337 2338 2339 2340 2341 2342 2343 2344 2345 2346 2347 2348 2349 2350 2351 2352 2353 2354 2355 2356 2357 2358 2359 2360 2361 2362 2363 2364 2365 2366 2367 2368 2369 2370 2371 2372 2373 2374 2375 2376 2377 2378 2379 2380 2381 2382 2383 2384 2385 2386 2387 2388 2389 2390 2391 2392 2393 2394 2395 2396 2397 2398 2399 2400 2401 2402 2403 2404 2405 2406 2407 2408 2409 2410 2411 2412 2413 2414 2415 2416 2417 2418 2419 2420 2421 2422 2423 2424 2425 2426 2427 2428 2429 2430 2431 2432 2433 2434 2435 2436 2437 2438 2439 2440 2441 2442 2443 2444 2445 2446 2447 2448 2449 	
--	--

FIGURE 3 (continued)

AGCTGGCGACGGGAGACAACCATGGACTTTGGTATGGAACCACACAGCCTCTTCACAGAC
 601 -----+-----+-----+-----+-----+-----+
 S W R R E T T M D F G M E P H S L F T D

GGACAGGTGCTGAGCATTTCCTGGGACCAGGAGACAGAGATGTGGCCTATTCCTGCATT
 661 -----+-----+-----+-----+-----+-----+
 G Q V L S I S L G P G D R D V A Y S C I

GTCTCCAACCCTGTCAGCTGGGACTTGGCCACAGTCACGCCCTGGGATAGCTGTCATCAT
 721 -----+-----+-----+-----+-----+-----+
 V S N P V S W D L A T V T P W D S C H H

GAGGCAGCACCCAGGGAAGGCCTCCTACAAAGATGTGCTGCTGGTGGTGGCCTGTCTCG
 781 -----+-----+-----+-----+-----+-----+
 E A A P G K A S Y K D V L L V V V P V S

CTGCTCCTGATGCTGGTTACTCTCTTCTCTGCCTGGCACTGGTGGCCCTGCTCAGGGAAA
 841 -----+-----+-----+-----+-----+-----+
 L L L M L V T L F S A W H W C P C S G K

AAGAAAAAGGATGTCCATGCTGACAGAGTGGGTCCAGAGACAGAGAACCCCTTGTGCAG
 901 -----+-----+-----+-----+-----+-----+
 K K K D V H A D R V G P E T E N P L V Q

GATCTGCCATAAAGGACAATATGAACTGATGCCTGGACTATCAGTAACCCCACTGCACAG
 961 -----+-----+-----+-----+-----+-----+
 D L P *

GCACACGATGCTCTGGGACATAACTGGTGCCTGGAAATCACCATGGTCCTCATATCTCCC
 1021 -----+-----+-----+-----+-----+-----+
 ATGGGAATCCTGTCTGCCTCGAAGGAGCAGCCTGGGCAGCCATCACACCACGAGGACAG

1081 -----+-----+-----+-----+-----+-----+
 GAAGCACCAGCACGTTTCACACCTCCCCCTTCCCTCTCCCATCTTCTCATATCCTGGCTC

1141 -----+-----+-----+-----+-----+-----+
 TTCTCTGGGCAAGATGAGCCAAGCAGAACATTCCATCCAGGACACTGGAAGTTCTCCAGG

1201 -----+-----+-----+-----+-----+-----+

FIGURE 4 (continued)

ATCCAGATCCATGGGGACATTAATAGTCCAAGGCATTCCCTCCCCCACCCTATTCATAA
1261 -----+-----+-----+-----+-----+-----+

AGTATTAACCAACTGGCACCAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA
1321 -----+-----+-----+-----+-----+-----+

AAAAAAAAAAAAAAGGGCGGCCGCCCCG
1381 -----+-----+----- 1408

FIGURE 4 (continued)

M	A	G	S	P	T	C	L	T	L	I	Y	I	L	W	Q	L	T	G	S
A	A	S	G	P	V	K	E	L	V	I	S	V	G	G	A	V	T	F	P
L	K	S	K	V	K	Q	V	D	S	I	V	W	T	F	N	T	T	P	L
V	T	I	Q	P	E	G	G	T	I	I	V	T	Q	N	R	N	R	E	R
V	D	F	P	D	G	G	Y	S	L	K	L	S	K	L	K	K	N	D	S
G	I	Y	Y	V	G	I	Y	S	S	S	L	Q	Q	P	S	T	Q	E	Y
V	L	H	V	Y	E	H	L	S	K	P	K	V	T	M	G	L	Q	S	N
K	N	G	T	C	V	T	N	L	T	C	C	M	E	H	G	E	E	D	V
I	Y	T	W	K	A	L	G	Q	A	A	N	E	S	H	N	G	S	I	L
P	I	S	W	R	W	G	E	S	D	M	T	F	I	C	V	A	R	N	P
V	S	R	N	F	S	S	P	I	L	A	R	K	L	C	E	G	A	A	D
D	P	D	S	S	M	V	L	L	C	L	L	L	V	P	L	L	A	S	L
F	V	L	G	L	F	L	W	F	L	K	R	E	R	Q	E	E	Y	I	E
E	K	K	R	V	D	I	C	R	E	T	P	N	I	C	P	H	S	G	E
N	T	E	Y	D	T	I	P	H	T	N	R	T	I	L	K	E	D	P	A
N	T	V	Y	S	T	V	E	I	P	K	K	M	E	N	P	H	S	L	L
T	M	P	D	T	P	R	L	F	A	Y	E	N	V	I	*				

FIGURE 5

M A V S R A P T P D S A C Q R M V W L F P L V F C L
 S G S E V S Q S S N S I D I Q M N G V L G E S V A V L P I
 K L P A G K I S A N I I M G W E A S Q I E R L S T Q S I L
 N L S A G K I S A N I I M G W E A S Q I E R L S T Q S I L
 Q Y I H L N L R V C F V I V S R N C T V S G D Q L T E T A
 G I G N L S V T S I I S L C I S K G V C W L T S F V C L V
 S M T P T L S I Q H I L C I S K G V C W L T S F V C L V
 L V T R E P S Q E A P E K T G Y N Q P I T L S M V N T Y I
 S *

FIGURE 6



FIGURE 8

Tissue Distribution of Apex1 Expression

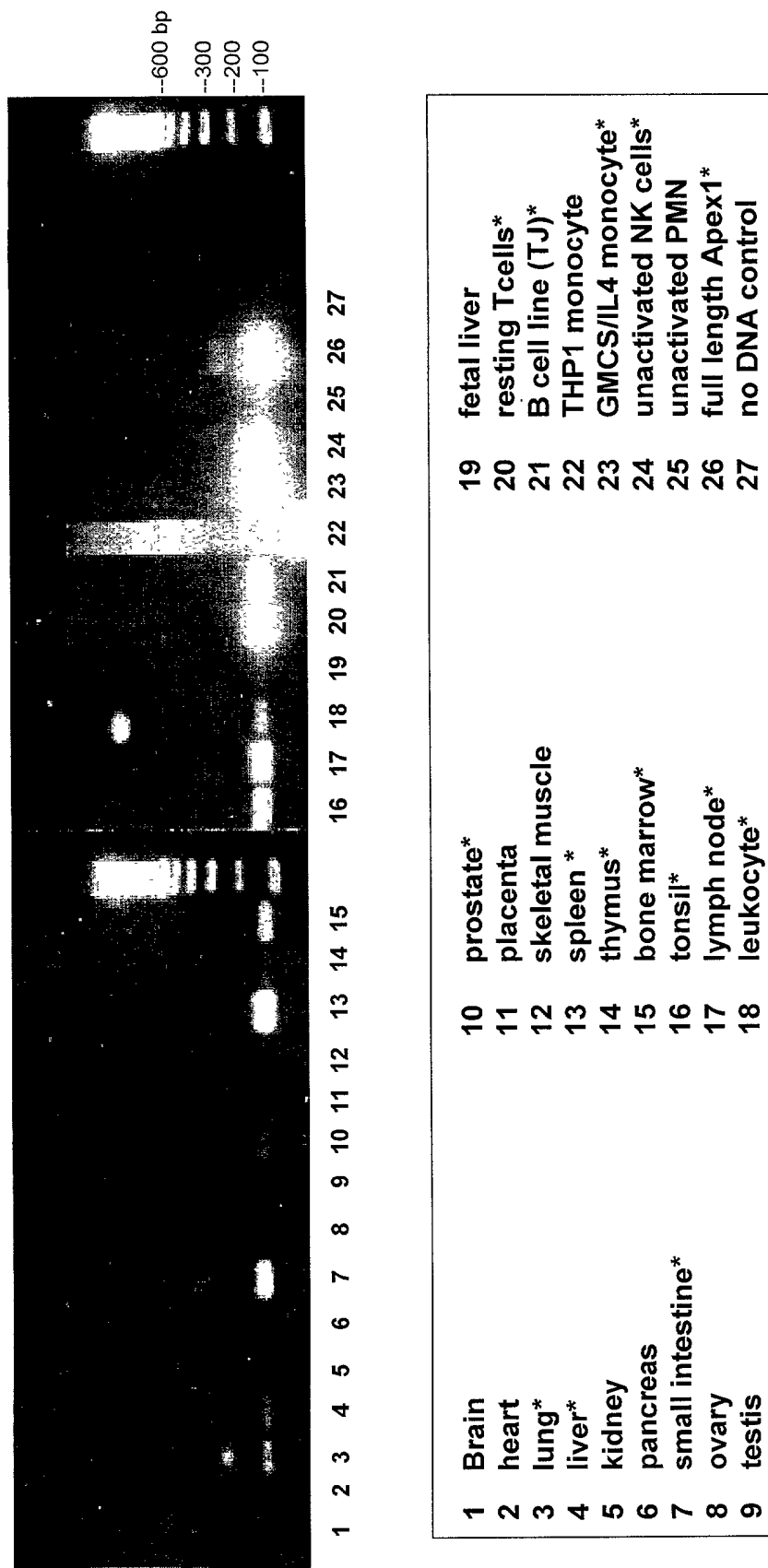


FIGURE 9

Peptides in APEX-1Ig

1 **MAGSPTCLTL IYILWQLTGS** **AAS**GPVKELV GSVGGAVTFP LKSKVKQVDS
51 IVWTFNTTPL VTIQPEGGTI IVTQNRNRER VDFPDGGGYSL KLSKLKKNDS
101 GIYYVGIYSS SLQQPSTQEY VLHVEHLSK PKVTMGLQSN KNGTCVTNLT
151 CCMEHGEEVD IYTWKALGQA ANESHNGSIL PISWRWGESD MTFICVARNP
201 VSRNFSSPIL ARKLCEGAAD DPDSS HP humanIgG1 H-CH2-CH3

Bold- Predicted signal sequence, which will be cleaved in mature protein HP - junction sequence resulting from the BamH1 enzyme site.

FIGURE 10

Peptides in APEX-2mIg

1 **MAVSRAPTPD** **SACQRMVWLF** **PLVFCLGSGS** EVSQSSSDPQ LMNGVLGESA
51 VLPLKLPAGK IANIIIWNYE WEASQVTALV INLSNPESPQ IMNTDVKKRL
101 NITQSYSLQI SNLTMADTGS YTAQITTKDS EVITFKYILR VFERLGNLET
151 TNYTLLLENG TCQIHLACVL KNQSQTVSVE WQATGNISLG GPNVTIFWDP
201 RNSGDQTYVC RAKNAVSNLS VSVSTQSLCK GVLTNPPW HP - murine
IgG2a H-Ch2-CH3

Bold- Predicted signal sequence, which will be cleaved in the mature protein HP - junction sequence resulting from the BamH1 enzyme site.

FIGURE 11

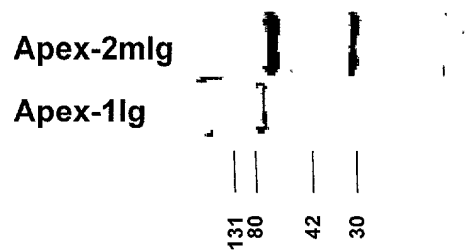


FIGURE 12

Downloaded from www.sciencedirect.com

Sf9
Cos

148 —

60 —



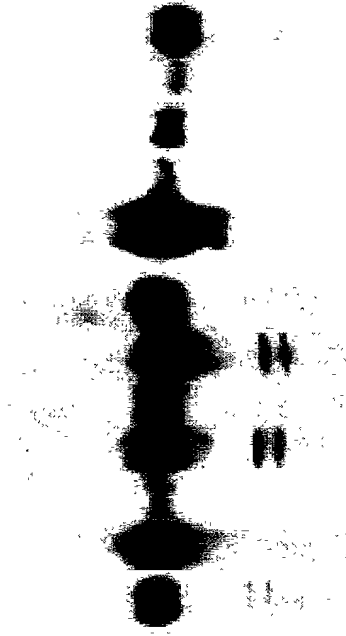
FIGURE 13

Apex1 Antibody Panel

Reduced

13 30 31 34 35 36 40 66 67 68 71 73

204 kb--
121--
78--
40--
30--



Non reduced

13 30 31 34 35 36 40 66 67 68 69 71 73

204--
121--
78--
40--
30--

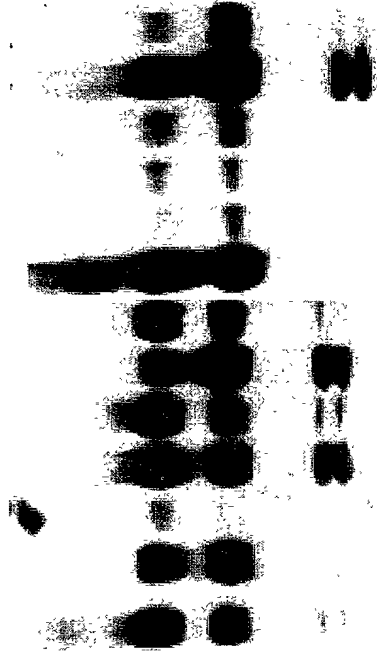


FIGURE 14

FLAG-APEX-1

MPMGS**LQPLATLYLLGMLVASCLG****DYKDDDDK****SGPVKELVGSVGGAVTFP**
LKS~~K~~V~~K~~Q~~V~~DSIVWTFNTT~~P~~LV~~T~~IQ~~P~~EGGTII~~V~~TQ~~N~~R~~N~~R~~E~~R~~V~~DFPDGGYSLKLSKLKKNDS
GIYYVGIYSSSLQQPSTQEYVLHVYEHLSKPKVTMGLQSNKNGTCVTNLTCCMEHGEEDV
IYTWKALGQAANESHNGSILPISWRWGESDMTFICVARNPVSRNFSSPILARKLCEGAAD
DPDSSMVLLCLLLVPLLLSLFVLGLFLWFLKRERQEYIEEKKRVDICRETPNICPHSGE
NTEYDTIPHTNRTILKEDPANTVYSTVEIPKKMENPHSLLTMPDTPRLFAYENVI*

MPMGS**LQPLATLYLLGMLVASCLG** sequence from human CD5 signal peptide,
DYKDDDDK is the FLAG peptide

FIGURE 15

FLAG-APEX-2

MPMGS**LQPLATLYLLGMLVASCLG****DYKDDDDK**SEVSQSSSDPQLMNGVLGESAVLPLKLPAGKIANIIWNYEWEASQVTALVINLSNPESPQIMNTDVKKRLNITQSYSLQISNLTMA DTGSYTAQITTKDSEVITFKYILRVFERLGNLETTNYTLLLENGTCQIHLACVLKNQSQTVSVVEWQATGNISLGGPNVTIFWDPRNSGDQTYVCRAKNAVSNLSVSVSTQSLCKGVLTNPPWNAVWFMTTISIISAVILIFVCWSIHVWKRRGSLPLTSQHPESSQSTDGPGSPGNTVYAQVTRPMQEMKIPKPIKNDSTIYSIVNHSREETVALTGYNQPITLKVNTLINYS*

MPMGS**LQPLATLYLLGMLVASCLG** sequence from human CD5 signal peptide,
DYKDDDDK is the FLAG peptide

FIGURE 16

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